

## SEQUENCE LISTING

<110> UNIVERSITY OF ROCHESTER

<120> Hormone Response Element Binding  
Transregulators

<130> 21108.0032P1

<150> 60/508,763

<151> 2003-10-03

<160> 84

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 6

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 1  
agaaca 6

<210> 2

<211> 6

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 2  
aggta 6

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<221> misc\_feature

<222> 7,8,9

<223> n = g, a, c or t(u)

<400> 3  
agaacanmt gttct 15

<210> 4

<211> 13

<212> DNA

<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct  
  
<221> misc\_feature  
<222> 7  
<223> n = g, a, c, or t(u)  
  
<400> 4  
aggtaaaaaa tca 13  
  
<210> 5  
<211> 12  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct  
  
<400> 5  
aggcatgac ct 12  
  
<210> 6  
<211> 13  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct  
  
<400> 6  
ggtcacggtg gcc 13  
  
<210> 7  
<211> 13  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct  
  
<400> 7  
ggtgacccttg acc 13  
  
<210> 8  
<211> 13  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct  
  
<400> 8  
ggtcaaggcg atc 13

```
<210> 9
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<221> misc_feature
<222> 6,7,8
<223> n = g, a, c or t(u)

<400> 9
ggtcannntg acc 13

<210> 10
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10
gggcattcggt acc 13

<210> 11
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 11
ggtcgccagg acc 13

<210> 12
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 12
ggtcaggctg gtc 13

<210> 13
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct
```

<400> 13  
ggccgggctg acc 13

<210> 14  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 14  
ggccgggctg acc 13

<210> 15  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 15  
ggccacgatg aca 13

<210> 16  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 16  
ggtggccctg acc 13

<210> 17  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 17  
ggtcaaggtg acc 13

<210> 18  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 18  
ggtcatggtg acc 13

<210> 19  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 19  
gcaggagctg acc 13

<210> 20  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 20  
ggtcagcgtg gcc 13

<210> 21  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 21  
aatcagactg act 13

<210> 22  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 22  
ggtcaggctg gtc 13

<210> 23  
<211> 69  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 23  
Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr  
1 5 10 15  
Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile  
20 25 30  
Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile  
35 40 45  
Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys  
50 55 60  
Tyr Glu Val Gly Met  
65

<210> 24

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 24

Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys  
1 5 10 15  
His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser  
20 25 30  
Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile  
35 40 45  
Lys Arg Ser  
50

<210> 25

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 25

Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His  
1 5 10 15  
Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser  
20 25 30  
Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr  
35 40 45  
Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys  
50 55 60  
Cys Tyr Glu Val Gly Met  
65 70

<210> 26

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =

## synthetic construct

&lt;400&gt; 26

Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val Arg  
1 5 10 15  
Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly  
20 25

&lt;210&gt; 27

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 27

Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His  
1 5 10 15  
Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala  
20 25 30  
Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile  
35 40 45  
Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys  
50 55 60  
Cys Leu Gln Ala Gly Met Asn Leu Glu Ala  
65 70

&lt;210&gt; 28

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 28

Arg Lys Thr Lys Lys Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly  
1 5 10 15  
Val Ser Gln Glu Thr Ser Glu Asn Pro Gly Asn Lys Thr Ile Val Pro  
20 25 30  
Ala Thr Leu Pro Gln Leu Thr Pro Thr Gly Arg  
35 40

&lt;210&gt; 29

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 29

Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His  
1 5 10 15  
Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala  
20 25 30

Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr  
35 40 45  
Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys  
50 55 60  
Cys Tyr Glu Ala Gly Met Thr Leu  
65 70

<210> 30  
<211> 56  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 30  
Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu  
1 5 10 15  
Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr Gln Lys  
20 25 30  
Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu  
35 40 45  
Asn Val Leu Glu Ala Ile Ala Arg  
50 55

<210> 31  
<211> 72  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 31  
Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His  
1 5 10 15  
Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala  
20 25 30  
Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile  
35 40 45  
Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu Arg Lys  
50 55 60  
Cys Cys Gln Ala Gly Met Val Leu  
65 70

<210> 32  
<211> 53  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 32  
Gly Gly Arg Lys Phe Lys Lys Phe Asn Lys Val Arg Val Val Arg Ala  
1 5 10 15  
Leu Asp Ala Val Ala Leu Pro Gln Pro Val Gly Val Pro Asn Glu Ser  
20 25 30

Gln Ala Leu Ser Gln Arg Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln  
35 40 45

Leu Ile Pro Pro Leu  
50

<210> 33  
<211> 72  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 33  
Lys Asp Glu Leu Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His  
1 5 10 15  
Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr  
20 25 30  
Ile Gln Lys Asn Leu His Pro Ser Tyr Ser Cys Lys Tyr Glu Gly Lys  
35 40 45  
Cys Val Ile Asp Lys Val Thr Arg Asn Gln Cys Gln Glu Cys Arg Phe  
50 55 60  
Lys Lys Cys Ile Tyr Val Gly Met  
65 70

<210> 34  
<211> 63  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 34  
Ala Thr Asp Leu Val Leu Asp Asp Ser Lys Arg Leu Ala Lys Arg Lys  
1 5 10 15  
Leu Ile Glu Glu Asn Arg Glu Lys Arg Arg Arg Glu Glu Leu Gln Lys  
20 25 30  
Ser Ile Gly His Lys Pro Glu Pro Thr Asp Glu Glu Trp Glu Leu Ile  
35 40 45  
Lys Thr Val Thr Glu Ala His Val Ala Thr Asn Ala Gln Gly Ser  
50 55 60

<210> 35  
<211> 70  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 35  
Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His  
1 5 10 15  
Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr  
20 25 30

Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp Cys Leu  
35 40 45  
Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys  
50 55 60  
Cys Leu Ala Met Gly Met  
65 70

<210> 36

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 36

Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn  
1 5 10 15  
Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met Pro Val  
20 25 30  
Glu Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr  
35 40 45  
Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser  
50 55

<210> 37

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 37

Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser Gly Tyr His  
1 5 10 15  
Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser  
20 25 30  
Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg Asp Lys Asn Cys Ile  
35 40 45  
Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Lys  
50 55 60  
Cys Phe Glu Val Gly Met Ser Lys  
65 70

<210> 38

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 38

Glu Ser Val Arg Asn Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys  
1 5 10 15

Pro Glu Cys Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu  
20 25 30  
Ile Glu Lys Val Arg Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys  
35 40 45  
Gln Leu Gly Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser  
50 55 60  
Leu Asp Ile Asp Leu  
65

<210> 39  
<211> 70  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 39  
Arg Ile Cys Gly Val Cys Gly Asp Arg Ala Thr Gly Phe His Phe Asn  
1 5 10 15  
Ala Met Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Met Lys  
20 25 30  
Arg Lys Ala Leu Phe Thr Cys Pro Phe Asn Gly Asp Cys Arg Ile Thr  
35 40 45  
Lys Asp Asn Arg Arg His Cys Gln Ala Cys Arg Leu Lys Arg Cys Val  
50 55 60  
Asp Ile Gly Met Met Lys  
65 70

<210> 40  
<211> 65  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 40  
Glu Phe Ile Leu Thr Asp Glu Glu Val Gln Arg Lys Arg Glu Met Ile  
1 5 10 15  
Leu Lys Arg Lys Glu Glu Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys  
20 25 30  
Leu Ser Glu Glu Gln Gln Arg Ile Ile Ala Ile Leu Leu Asp Ala His  
35 40 45  
His Lys Thr Tyr Asp Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro  
50 55 60

Pro  
65

<210> 41  
<211> 134  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 41

Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly  
 1               5               10               15  
 Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu  
 20               25               30  
 Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr  
 35               40               45  
 Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln  
 50               55               60  
 Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr  
 65               70               75               80  
 Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp  
 85               90               95  
 Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu  
 100              105              110  
 Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala  
 115              120              125  
 Leu Leu Ser Gln Ile Ser  
 130

&lt;210&gt; 42

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 42

Lys Val Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu  
 1               5               10               15  
 Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe  
 20               25               30  
 Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr  
 35               40               45  
 Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu  
 50               55               60  
 Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly  
 65               70               75               80  
 Glu Phe Pro Gly Ile Arg Arg  
 85

&lt;210&gt; 43

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 43

Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala  
 1               5               10               15  
 Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser  
 20               25               30  
 Met Leu Pro  
 35

<210> 44  
<211> 90  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 44  
Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe  
1 5 10 15  
Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp  
20 25 30  
Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys  
35 40 45  
Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu  
50 55 60  
Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His  
65 70 75 80  
Gln Glu Thr His Pro Asp Ser Glu Thr Ala  
85 90

<210> 45  
<211> 595  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 45  
Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His  
1 5 10 15  
Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys  
20 25 30  
Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys  
35 40 45  
Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala  
50 55 60  
Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr  
65 70 75 80  
Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly  
85 90 95  
Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His  
100 105 110  
Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val  
115 120 125  
Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala  
130 135 140  
Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly  
145 150 155 160  
Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met  
165 170 175  
Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala  
180 185 190  
Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe  
195 200 205  
Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr  
210 215 220

Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys  
 225                    230                    235                    240  
 Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg  
 245                    250                    255  
 Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp  
 260                    265                    270  
 Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala  
 275                    280                    285  
 Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn  
 290                    295                    300  
 Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu  
 305                    310                    315                    320  
 Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro  
 325                    330                    335  
 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg  
 340                    345                    350  
 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val  
 355                    360                    365  
 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu  
 370                    375                    380  
 Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val  
 385                    390                    395                    400  
 Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys  
 405                    410                    415  
 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser  
 420                    425                    430  
 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Phe Val Cys Leu  
 435                    440                    445  
 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser  
 450                    455                    460  
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp  
 465                    470                    475                    480  
 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr  
 485                    490                    495  
 Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser  
 500                    505                    510  
 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met  
 515                    520                    525  
 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Met Leu  
 530                    535                    540  
 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val  
 545                    550                    555                    560  
 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser  
 565                    570                    575  
 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro  
 580                    585                    590  
 Ala Thr Val  
 595

<210> 46  
 <211> 2092  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 46  
 gaattccaaa attgtgatgt ttcttgatt tttgatgaag gagaaatact gtaatgatca  
 ctgtttacac tatgtacact tttaggcagc cctttttagc gttataaaaa ctgaaaagcac

60

120

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| accggaccccg | caggctcccgg | gggcaggggcc | ggggccagag  | ctcgcgtgtc  | ggcgggacat  | 180  |
| gcgctgcgtc  | gcctctaacc  | tcgggtctgt  | ctcttttcc   | aggtgcccg   | ccggtttctg  | 240  |
| agcattctgc  | cctgcggggaa | cacggctctgc | accctgcccg  | cggccacgga  | ccatgaccat  | 300  |
| gaccctccac  | accaaagcat  | ctgggatggc  | cctactgcat  | cagatccaag  | ggaacgagct  | 360  |
| ggagccccctg | aaccgtccgc  | agctcaagat  | ccccctggag  | cggcccccgg  | gcgagggtgt  | 420  |
| cctggacagc  | agcaagcccc  | ccgtgtacaa  | ctaccccgag  | ggcgcgcgcct | acgagttcaa  | 480  |
| cgccgcggcc  | gccgccaacg  | cgcaggctca  | cgttcagacc  | ggccctccct  | acggcccccgg | 540  |
| gtctgaggct  | ggggcggtcg  | gctccaacgg  | cctggggggt  | tccccccac   | tcaacagcgt  | 600  |
| gtctccgagc  | ccgctgatgc  | tactgcaccc  | gccgcgcgag  | ctgtcgccct  | tcctgcagcc  | 660  |
| ccacggccag  | caggtgcacct | actacctgga  | gaacgagccc  | agcggctaca  | cggtgccgca  | 720  |
| ggccggcccg  | ccggcattct  | acagggccaaa | ttcagataat  | cgacgcccagg | gtggcagaga  | 780  |
| aagattggcc  | agtaccaatg  | acaaggaaag  | tatggctatg  | gaatctgcca  | aggagactcg  | 840  |
| ctactgtgca  | gtgtcaatg   | actatgcttc  | aggctaccat  | tatggagtct  | ggtcctgtga  | 900  |
| gggctgcaag  | gccttcttca  | agagaagtat  | tcaaggacat  | aacgactata  | tgtgtccagc  | 960  |
| caccaaccag  | tgcaccattg  | ataaaaaacag | gaggaagagc  | tgccaggcct  | gccggctccg  | 1020 |
| caaatgtac   | gaagtgggaa  | tgatgaaagg  | ttggatacga  | aaagaccgaa  | gaggagaggag | 1080 |
| aatgttggaa  | cacaagcgcc  | agagagatga  | ttggggagggc | aggggtgaag  | ttgggtctgc  | 1140 |
| tggagacatg  | agagctgcca  | acctttggcc  | aagcccgctc  | atgatcaaac  | gctctaagaa  | 1200 |
| gaacagcctg  | gccttgcctc  | tgacggccga  | ccagatggc   | agtgccttgt  | tggatgtga   | 1260 |
| gccccccata  | ctctattccg  | agtatgatcc  | taccagaccc  | ttcagtgaag  | tttcgatgtat | 1320 |
| gggcttactg  | accaacctgg  | cagacaggga  | gctggttcac  | atgatcaact  | gggcgaagag  | 1380 |
| gggtgccaggc | tttggatt    | tgaccctcca  | tgatcagggtc | cacccctctag | aatgtgcctg  | 1440 |
| gctagagatc  | ctgatgattg  | gtctcgctg   | gcgctccatg  | gagcaccagg  | tgaagctact  | 1500 |
| gtttgctcct  | aacttgctct  | tggacaggaa  | ccagggaaaa  | tgttagagg   | gcatggtgga  | 1560 |
| gatttcgac   | atgctgctgg  | ctacatcata  | tcgggtccgc  | atgatgaatc  | tgcaaggagaa | 1620 |
| ggagtttgg   | tgcctcaaatt | ctattatTTT  | gcttaattct  | ggagtgtaca  | catttctgtc  | 1680 |
| cagcacccctg | aagtctctgg  | aagagaagga  | ccatatccac  | cgagtcctgg  | acaagatcac  | 1740 |
| agacactttg  | atccacctga  | tggccaaaggc | aggcctgacc  | ctgcagcagc  | agcaccagcg  | 1800 |
| gctggcccgag | ctccctcctca | tcctctccca  | catcaggcac  | atgagtaaca  | aaggcatgg   | 1860 |
| gcatctgtac  | agcatgaagt  | gcaagaacgt  | ggtgcgcctc  | tatgacctgc  | tgctggagat  | 1920 |
| gctggacgcc  | caccgcctac  | atgcgcctac  | tagccgtgga  | ggggcatccg  | tggaggagac  | 1980 |
| ggaccAAAGC  | cacttggcca  | ctgcgggctc  | tacttcatcg  | catttcttgc  | aaaagtatta  | 2040 |
| catcacqqqq  | qaggcqaqaq  | gtttccctgc  | cacagtctga  | gagctccctg  | gc          | 2092 |

```
<210> 47
<211> 207
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

```

<400> 47
actcgctact gtgcagtgtg caatgactat gtttcaggct accattatgg agtctggtcc      60
tgtgagggct gcaaggcctt cttcaagaga agtattcaag gacataacga ctatatgtgt     120
ccagccacca accagtgcac cattgataaa aacaggagga agagctgccca ggcctgccgg     180
ctccgcaaat gctacgaagt gggaaatg                                         207

```

```
<210> 48
<211> 153
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 48 atgaaaagggtg ggatacgaaa agaccgaaga ggagggagaa tggtaaaaca caagcgccag 60  
aqaqatqatq qggagggcag gggtaagtg gggctgtctg gagacatgag agctgccaac 120

ctttggccaa gcccgcctcat gatcaaacgc tct

153

<210> 49  
<211> 530  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 49  
Met Asp Ile Lys Asn Ser Pro Ser Ser Leu Asn Ser Pro Ser Ser Tyr  
1               5               10               15  
Asn Cys Ser Gln Ser Ile Leu Pro Leu Glu His Gly Ser Ile Tyr Ile  
20               25               30  
Pro Ser Ser Tyr Val Asp Ser His His Glu Tyr Pro Ala Met Thr Phe  
35               40               45  
Tyr Ser Pro Ala Val Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn  
50               55               60  
Leu Glu Gly Gly Pro Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp  
65               70               75               80  
Pro Thr Pro Gly His Leu Ser Pro Leu Val Val His Arg Gln Leu Ser  
85               90               95  
His Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser  
100              105              110  
Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val  
115              120              125  
Ser Gly Asn Arg Cys Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg  
130              135              140  
Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His  
145              150              155              160  
Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser  
165              170              175  
Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr  
180              185              190  
Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys  
195              200              205  
Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys  
210              215              220  
Gly Tyr Arg Leu Val Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His  
225              230              235              240  
Cys Ala Gly Lys Ala Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg  
245              250              255  
Glu Leu Leu Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu  
260              265              270  
Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro  
275              280              285  
Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys  
290              295              300  
Glu Leu Val His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val  
305              310              315              320  
Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met  
325              330              335  
Glu Val Leu Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly  
340              345              350  
Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys  
355              360              365  
Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr  
370              375              380

Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val  
 385 390 395 400  
 Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala  
 405 410 415  
 Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala  
 420 425 430  
 Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser  
 435 440 445  
 Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His  
 450 455 460  
 Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys  
 465 470 475 480  
 Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Glu Met Leu Asn  
 485 490 495  
 Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys  
 500 505 510  
 Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln  
 515 520 525  
 Ser Gln  
 530

<210> 50  
 <211> 2011  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 50  
 tttcagtttc tccagctgct ggcttttgg acacccactc ccccgcagg aggcaagg 60  
 aagcgcggag gctgcgagaa ataactgcct cttgaaaactt gcagggcgaa gagcaggcgg 120  
 cgagcgctgg gccggggagg gaccacccga gctgcgacgg gctctgggc tgccggcg 180  
 ggctggcgcc cggagcctga gctgcagggag gtgcgtcgc ttccctcaac aggtggcg 240  
 ggggcgcgcg cggggagacc cccccataatg cggggaaaagc acgtgtccgc atttttagaga 300  
 aggcaaggcc ggtgttta tctgcaagcc attatacttg cccacgaatc tttgagaaca 360  
 ttataatgac ctttgtcct cttcttgc aa ggtgtttct cagctgttat ctcaagacat 420  
 gatatataaa aactcaccat ctgccttaa ttctccctcc tcctacaact gcagtcaatc 480  
 catcttaccc ctggagcacg gctccatata cataccttcc tcctatgttag acagccacca 540  
 tgaatatcca gccatgacat tctatagccc tgctgtgatg aattacagca ttcccagcaa 600  
 tgtcaacttac ttggaaagg 660  
 ggcctggcg 660  
 gcaagaccaca 660  
 ttataatgac ctttgtcct cttcttgc aa ggtgtttct cagctgttat ctcaagacat 720  
 gatatataaa aactcaccat ctgccttaa ttctccctcc tcctacaact gcagtcaatc 720  
 acctcaaaag agtccctgg 780  
 gtgaagcaag atcgctagaa cacaccttac ctgtaaacag 780  
 agagacactg aaaagaagg ttagtggaa ccgttgcgc 840  
 agccctgtta ctggtccagg 840  
 ttcaaaagagg gatgctact tctgcgtgt ctgcagcgat tacgcacatc gatatacta 900  
 tgtagtctgg 960  
 tgctgtgaag gatgttgg 960  
 ctttttaaa agaaggattt 960  
 tgattatatt tgccagcta caaatcagtg tacaatcgat aaaaacccgc gcaagagctg 1020  
 ccaggcctgc cgacttcgga agtggatcga agtggaaatg gtgaagtgtg gctcccg 1080  
 agagagatgt gggtaccg 1140  
 gcccggcaag gccaagagaa gtggcgcc 1200  
 cggccctgagc cccgagcagc tagtgcac cctctgg 1260  
 gatcagccgc cccagtcgc ctttacccga ggcctccatg atgatgtccc tgaccaagtt 1320  
 gggccgacaag gagttgtac acatgatcag ctggccaa 1380  
 gctcagccctg ttcgaccaag tgcggctt ggagagctgt 1440  
 ggggctgtatg tggcgctcaa ttgaccaccc cggcaagctc 1500  
 tctggacagg gatgaggg 1560  
 gggcaactact tcaagtttc gagagttaa actccaacac 1620  
 gggccatgatc ctgcctcaatt ccagatgt 1680  
 cggcggccgg aagctggctc acttgcgtaa cggccgtgacc 1740  
 tgccaaagagc ggcacatcctt cccagcagca atccatgcgc 1800

|   |      |
|---|------|
| cctgtcccac gtcaggcatg cgagtaacaa gggcatggaa catctgctca acatgaagtg           | 1860 |
| caaaaatgtg gtcccagtgt atgacctgt gctggagatg ctgaatgcc acgtgcttcg             | 1920 |
| cgggtgcaag tcctccatca cggggtccga gtgcagcccg gcagaggaca gtaaaagcaa           | 1980 |
| agagggctcc cagaaccac agtctcagtg a   | 2011 |
| <br>  |      |
| <210> 51  |      |
| <211> 210   |      |
| <212> DNA   |      |
| <213> Artificial Sequence   |      |
| <br>  |      |
| <220>   |      |
| <223> Description of Artificial Sequence; note =                            |      |
| synthetic construct   |      |
| <br>  |      |
| <400> 51  |      |
| gatgctcaact tctgcgctgt ctgcagcgat tacgcacatcg gatatcacta tggagtctgg         | 60   |
| tctgtgtgaag gatgtaaaggc cttttttaaa agaagcattc aaggacataa tgatttatatt        | 120  |
| tgtccagcta caaatcagtg tacaatcgat aaaaaccggc gcaagagctg ccaggcctgc           | 180  |
| cgacttcggaa agtgttacga agtggaaatg   | 210  |
| <br>  |      |
| <210> 52  |      |
| <211> 87  |      |
| <212> DNA   |      |
| <213> Artificial Sequence   |      |
| <br>  |      |
| <220>   |      |
| <223> Description of Artificial Sequence; note =                            |      |
| synthetic construct   |      |
| <br>  |      |
| <400> 52  |      |
| gtgaagtgtg gctcccgag agagagatgt gggtaccgccc ttgtgcggag acagagaagt           | 60   |
| gccgacgagc agctgcactg tgccggc   | 87   |
| <br>  |      |
| <210> 53  |      |
| <211> 777   |      |
| <212> PRT   |      |
| <213> Artificial Sequence   |      |
| <br>  |      |
| <220>   |      |
| <223> Description of Artificial Sequence; note =                            |      |
| synthetic construct   |      |
| <br>  |      |
| <400> 53  |      |
| Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser             |      |
| 1                       5                       10                       15 |      |
| Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr             |      |
| 20                      25                      30                          |      |
| Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu             |      |
| 35                      40                      45                          |      |
| Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp             |      |
| 50                      55                      60                          |      |
| Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys             |      |
| 65                      70                      75                      80  |      |
| Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys             |      |
| 85                      90                      95                          |      |
| Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu             |      |
| 100                    105                     110                          |      |
| Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn             |      |
| 115                    120                     125                          |      |
| Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser             |      |
| 130                    135                     140                          |      |

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His  
 145 150 155 160  
 Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr  
 165 170 175  
 Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp  
 180 185 190  
 Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr  
 195 200 205  
 Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu  
 210 215 220  
 Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn  
 225 230 235 240  
 Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys  
 245 250 255  
 Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr  
 260 265 270  
 Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr  
 275 280 285  
 Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala  
 290 295 300  
 Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser  
 305 310 315 320  
 Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met  
 325 330 335  
 Asn Thr Ala Ser Leu Ser Gln Gln Asp Gln Lys Pro Ile Phe Asn  
 340 345 350  
 Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln  
 355 360 365  
 Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro  
 370 375 380  
 Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro  
 385 390 395 400  
 Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro  
 405 410 415  
 Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His  
 420 425 430  
 Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala  
 435 440 445  
 Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile  
 450 455 460  
 Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys  
 465 470 475 480  
 Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys  
 485 490 495  
 Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser  
 500 505 510  
 Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu  
 515 520 525  
 Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu  
 530 535 540  
 Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met  
 545 550 555 560  
 Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys  
 565 570 575  
 Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln  
 580 585 590  
 Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala Phe Ala Leu  
 595 600 605  
 Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala  
 610 615 620

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asp | Leu | Ile | Ile | Asn | Glu | Gln | Arg | Met | Thr | Leu | Pro | Cys | Met | Tyr |
| 625 |     |     |     |     | 630 |     |     |     | 635 |     |     |     |     |     | 640 |
| Asp | Gln | Cys | Lys | His | Met | Leu | Tyr | Val | Ser | Ser | Glu | Leu | His | Arg | Leu |
|     |     |     |     |     | 645 |     |     |     | 650 |     |     |     |     |     | 655 |
| Gln | Val | Ser | Tyr | Glu | Glu | Tyr | Leu | Cys | Met | Lys | Thr | Leu | Leu | Leu |     |
|     |     |     |     | 660 |     |     |     | 665 |     |     |     |     |     |     | 670 |
| Ser | Ser | Val | Pro | Lys | Asp | Gly | Leu | Lys | Ser | Gln | Glu | Leu | Phe | Asp | Glu |
|     |     |     |     | 675 |     |     |     | 680 |     |     |     |     |     |     | 685 |
| Ile | Arg | Met | Thr | Tyr | Ile | Lys | Glu | Leu | Gly | Lys | Ala | Ile | Val | Lys | Arg |
|     |     | 690 |     |     |     | 695 |     |     |     | 700 |     |     |     |     |     |
| Glu | Gly | Asn | Ser | Ser | Gln | Asn | Trp | Gln | Arg | Phe | Tyr | Gln | Leu | Thr | Lys |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Leu | Leu | Asp | Ser | Met | His | Glu | Val | Val | Glu | Asn | Leu | Leu | Asn | Tyr | Cys |
|     |     |     |     |     | 725 |     |     |     | 730 |     |     |     |     |     | 735 |
| Phe | Gln | Thr | Phe | Leu | Asp | Lys | Thr | Met | Ser | Ile | Glu | Phe | Pro | Glu | Met |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     |     |     | 750 |
| Leu | Ala | Glu | Ile | Ile | Thr | Asn | Gln | Ile | Pro | Lys | Tyr | Ser | Asn | Gly | Asn |
|     |     |     |     | 755 |     |     |     | 760 |     |     |     |     |     |     | 765 |
| Ile | Lys | Lys | Leu | Leu | Phe | His | Gln | Lys |     |     |     |     |     |     |     |
|     |     |     | 770 |     |     |     |     | 775 |     |     |     |     |     |     |     |

```
<210> 54
<211> 4788
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

|   |  |      |
|---|--|------|
| <400> 54  |  | 60   |
| tttttagaaa aaaaaaatat attccctcc tgctccttct gcgttcacaa gctaaggtgt    |  | 120  |
| ttatctggc tcgcccggga actgcggacg gtggcgggca agcggctct ctgccagagt     |  | 180  |
| tgatattcac ttagggactc caaagaatca ttaactccctg gttagagaaga aaaccccagc |  | 240  |
| agtgtgcttg ctcaggagag gggagatgtg atggacttct ataaaaccct aagaggagga   |  | 300  |
| gctactgtga agtttctgc gtcttacccc tcaactggctg tcgcctctca atcagactcc   |  | 360  |
| aagcagcgaa gacttttggg tgatttcca aaaggctca tagcaatgc gcagcagcca      |  | 420  |
| gatctgtcca aagcagttc actctcaatg ggactgtata tggagagac agaaacaaaa     |  | 480  |
| gtgatggaa atgacctggg attcccacag cagggccaaa tcagcccttc ctgggggaa     |  | 540  |
| acagactta agcttttggg agaaagcatt gcaaaccctca ataggctcgac cagtgttcca  |  | 600  |
| gagaaccca agagttcagc atccactgct gtgtctgctg cccccacaga gaaggagttt    |  | 660  |
| ccaaaaactc actctgatgt atcttcagaa cagcaacatt tgaagggcca gactggcacc   |  | 720  |
| aacggtgcc atgtgaaatt gtataccaca gaccaaagca ccttgacat ttgcaggat      |  | 780  |
| ttggagttt ctctgggtc cccagtaaa gagacgaatg agactcctt gагатcага        |  | 840  |
| ctgttgatag ataaaaactg tttgcttct cctctggcgg gagaagacga ttcatccctt    |  | 900  |
| ttggaaggaa actcgaatga ggactgcaag cctctcattt tacccggacac taaacccaaa  |  | 960  |
| attaaggata atggagatct ggtttgcata agccccagta atgtAACACT gccccaaagt   |  | 1020 |
| aaaacagaaa aagaagattt catcgaactc tgcacccctg ggtaattaa gcaagagaaa    |  | 1080 |
| ctgggcacag ttactgtca ggcaagctt cctggagcaa atataattgg taataaaatg     |  | 1140 |
| tctgccattt ctgttcatgg tgtgagtacc tctggaggac agatgtacca ctatgacatg   |  | 1200 |
| aatacagcat cccttctca acagcaggat cagaagccta ttttaatgt cattccacca     |  | 1260 |
| attcccgtt gttccgaaaa ttggaatagg tgccaaggat ctggagatga caacttgact    |  | 1320 |
| tctctggga ctctgaactt ccctggctca acagttttt ctaatggcta ttcaagcccc     |  | 1380 |
| agcatgagac cagatgtaa ctctcctcca tccagctcct caacagcaac aacaggacca    |  | 1440 |
| cctcccaaactctggt gtgcctgtat gaagcttca gatgtcatta tggagtctta         |  | 1500 |
| acttgtggaa gctgtaaagt tttctcaaaa agagcagtgg aaggacagca caattaccta   |  | 1560 |
| tgtgtggaa ggaatgattt catcatcgat aaaattcgaa gaaaaaaactg cccagcatgc   |  | 1620 |
| cgctatcgaa aatgtctca ggctggaatg aacctggaa ctcgaaaaac aaagaaaaaa     |  | 1680 |
| ataaaaaggaa tttagcaggc cactacagga gtctcacaag aaacctctga aaatcctgg   |  | 1740 |
| aacaaacaa tagttctgc aacgttacca caactcaccc ctaccctggt gtcactgttg     |  | 1800 |
| gagggttattt aacctgaagt gttatatgca ggtatgata gctctgttcc agactcaact   |  |      |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tggaggatca  | tgactacgct  | caacatgtta  | ggagggcggc  | aagtgattgc  | agcagtgaaa  | 1860 |
| tggcaaagg   | caataccagg  | tttcaggaac  | ttacacctgg  | atgaccaaata | gaccctactg  | 1920 |
| cagtactcct  | ggatgttct   | tatggcatt   | gctctggggt  | ggagatcata  | tagacaatca  | 1980 |
| atgcaaacc   | tgctgttta   | tgctcctgat  | ctgattatta  | atgacgagag  | aatgactcta  | 2040 |
| ccctgcatgt  | acgaccaatg  | taaacacatg  | ctgtatgttt  | cctctgagtt  | acacaggcct  | 2100 |
| caggtatctt  | atgaagagta  | tctctgtatg  | aaaaccttac  | tgcttcttc   | ttcagttcct  | 2160 |
| aaggacggtc  | tgaagagcca  | agagctattt  | gatgaaatta  | aatgaccta   | catcaaagag  | 2220 |
| ctagaaaag   | ccattgtcaa  | gagggaaagga | aactccagcc  | agaactggca  | gcggtttat   | 2280 |
| caactgacaa  | aactcttgg   | ttctatgcat  | gaagtgggtg  | aaaatctcct  | taactattgc  | 2340 |
| ttccaaacat  | ttttggataa  | gaccatgagt  | attgaattcc  | ccgagatgtt  | agctgaaatc  | 2400 |
| atcacaatc   | agataccaaa  | atattcaaat  | ggaatataca  | aaaaacttct  | gtttcatcaa  | 2460 |
| aagtgactgc  | cttaataaga  | atggttgcct  | taaagaaaat  | cgaattaata  | gcttttattg  | 2520 |
| tataaactat  | cagtttgtcc  | tgttagaggtt | ttgtgttttt  | atttttattt  | gttttcatct  | 2580 |
| gttgggggt   | tttaaatacg  | cactacatgt  | ggtttataga  | gggccaagac  | ttggcaacag  | 2640 |
| aagcagttga  | gtcgtcatca  | cttttcagtg  | atggagagt   | agatggtgaa  | atttatttagt | 2700 |
| taatatatcc  | cagaaattag  | aaaccttaat  | atgtggacgt  | aatctccaca  | gtcaaagaag  | 2760 |
| gatggcacct  | aaaccaccag  | tgcccaaagt  | ctgtgtgatg  | aactttctct  | tcataacttt  | 2820 |
| tttcacagtt  | ggctggatga  | attttcttag  | actttctgtt  | gggttatccc  | ccccctgtat  | 2880 |
| agtaggata   | gcattttga   | tttatgcatg  | gaaacctgaa  | aaaaagttt   | caagtgtata  | 2940 |
| tcagaaaagg  | gaagttgtgc  | ctttatagc   | tattactgtc  | tggttttaac  | aatttcctt   | 3000 |
| atatttagt   | aactacgctt  | gctcattttt  | tcttacataa  | ttttttattt  | aagtttattgt | 3060 |
| acagctgttt  | aagatggca   | gctagttcgt  | agctttccca  | aataaactct  | aaacattaat  | 3120 |
| caatcatctg  | tgtaaaaatg  | ggttggtgct  | tctaacctga  | tggcacttag  | ctatcagaag  | 3180 |
| accacaaaaa  | ttgactcaaa  | tctccagttat | tcttgc当地    | aaaaaaaaaa  | aaaaagctca  | 3240 |
| tatTTTGTAT  | atatctgctt  | cagtggagaa  | ttatataatgt | tgtcaaattt  | aacagtccta  | 3300 |
| actggatata  | agcacatgt   | ccagtgcact  | gctgggtaaa  | ctgtggatga  | ttgttgcaaa  | 3360 |
| agactaattt  | aaaaaataac  | taccaagagg  | ccctgtctgt  | acctaacgcc  | ctatTTTGC   | 3420 |
| aatggctata  | tggcaagaaa  | gctggtaaaac | tattttgttt  | tcaggacctt  | ttgaagtagt  | 3480 |
| ttgtataact  | tcttaaaatg  | tgtgattcca  | gataaccagg  | tgtaaacacag | ctgagagact  | 3540 |
| ttaatcaga   | caaagtaatt  | cctctcacta  | aactttaccc  | aaaaactaaa  | tctctaataat | 3600 |
| ggcaaaaatg  | gctagacacc  | cattttcaca  | ttcccatctg  | tcaccaattt  | gttaatctt   | 3660 |
| cctgatggta  | cagggaaatgt | cagctactga  | ttttttgtat  | tttagaactgt | atgtcagaca  | 3720 |
| tccatgtttt  | taaaactaca  | catccctaaat | gtgtgccata  | gagtttaaca  | caagtccctgt | 3780 |
| gaatttcttc  | actgtgaaa   | attattttaa  | acaaaataga  | agctgttagt  | gccctttctg  | 3840 |
| tgtgcacctt  | accaacttcc  | tgtaaactca  | aaacttaaca  | tattttactaa | gccacaagaa  | 3900 |
| atttgcattt  | tattcaaggt  | ggccaaattn  | tttgc当地     | agaaaactgt  | aaatctaata  | 3960 |
| ttaaaaaat   | ggaacttcta  | atatattttt  | atatttagt   | atagttttag  | atataatata  | 4020 |
| tattggattt  | cactaatctg  | ggaagggaaag | ggctactgca  | gttttacatg  | caatttattt  | 4080 |
| aatatgattt  | aaaatagctt  | gtatagtgta  | aaataagaat  | gatttttaga  | tgagatttt   | 4140 |
| ttatcatgac  | atgttatata  | ttttttgtat  | gggtcaaaga  | aatgctgtat  | gataacctat  | 4200 |
| atgatttata  | gtttgtacat  | gcattcatac  | aggcagcgt   | ggtctcagaa  | accaaacagt  | 4260 |
| ttgctctagg  | ggaagggaaag | gtggagact   | ggtcctgtgt  | gcagtgaagg  | ttgctgaggc  | 4320 |
| tctgacccag  | tgagattaca  | gagggaaatgt | tcctctgcct  | cccattctga  | ccaccccttct | 4380 |
| cattccaaaca | gtgagttctgt | cagcgcaggt  | ttagttact   | caatctcccc  | ttgcactaaa  | 4440 |
| gtatgtaaag  | tatgtaaaca  | ggagacagga  | agggtgggtct | tacatccctt  | aaggcaccat  | 4500 |
| ctaatagcgg  | gttactttca  | catacagccc  | tccccccagca | gttgaatgac  | aacagaagct  | 4560 |
| tcagaagttt  | ggcaatagtt  | tgcatacgagg | taccagcaat  | atgtaaatag  | tgcagaatct  | 4620 |
| cataggttgc  | caataataca  | ctaatccctt  | tctatcctac  | aacaagagtt  | tatttccaaa  | 4680 |
| taaaatgagg  | acatgtttt   | gttttctttt  | aatgtttttt  | aatgttttatt | tggttattttc | 4740 |
| agatattttgg | agaaattattt | taataaaaaaa | acaatcattt  | gttttttg    |             | 4788 |

<210> 55  
<211> 222  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 55  
 cctcccaaac tctgcctgggt gtgctctgat gaagcttcag gatgtcatta tggagtctta 60  
 acttgtggaa gctgtaaagt tttcttcaaa agagcagtgg aaggacagca caattaccta 120  
 tgtgctggaa ggaatgattg catcatcgat aaaattcgaa gaaaaaaactg cccagcatgc 180  
 cgctatcgaa aatgtcttca ggctggaatg aacctggaag ct 222

<210> 56  
<211> 123  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 56  
cggaaaaacaa agaaaaaaat aaaaggaatt cagcaggcca ctacaggagt ctcacaagaa 60  
acctctgaaa atcctggtaa caaaaacaata gttcctgcaa cgttaccaca actcaccct 120  
acc 123

<210> 57  
<211> 734  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 57  
Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser  
1 5 10 15  
Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys  
20 25 30  
Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu  
35 40 45  
Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu  
50 55 60  
Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala  
65 70 75 80  
Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro  
85 90 95  
Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser  
100 105 110  
Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys  
115 120 125  
Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly  
130 135 140  
Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser  
145 150 155 160  
Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn  
165 170 175  
Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro His  
180 185 190  
Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala  
195 200 205  
Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu  
210 215 220  
His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala  
225 230 235 240

Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu  
                   245                  250                  255  
 Tyr Gly Pro Cys Gly  
                   260                  265                  270  
 Gly Glu  
                   275                  280                  285  
 Ala Glu Ala Val Ala Pro Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu  
                   290                  295                  300  
 Ala Gly Gln Glu Ser Asp Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly  
                   305                  310                  315                  320  
 Gly Met Val Ser Arg Val Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser  
                   325                  330                  335  
 Glu Met Gly Pro Trp Met Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met  
                   340                  345                  350  
 Arg Leu Glu Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe  
                   355                  360                  365  
 Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys  
                   370                  375                  380  
 His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg  
                   385                  390                  395                  400  
 Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys  
                   405                  410                  415  
 Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg  
                   420                  425                  430  
 Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys  
                   435                  440                  445  
 Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu Ala Ser Ser Thr Thr  
                   450                  455                  460  
 Ser Pro Thr Glu Glu Thr Thr Gln Lys Leu Thr Val Ser His Ile Glu  
                   465                  470                  475                  480  
 Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val Leu Glu Ala Ile Glu  
                   485                  490                  495  
 Pro Gly Val Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe  
                   500                  505                  510  
 Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val  
                   515                  520                  525  
 His Val Val Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His  
                   530                  535                  540  
 Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met  
                   545                  550                  555                  560  
 Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met  
                   565                  570                  575  
 Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys  
                   580                  585                  590  
 Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu  
                   595                  600                  605  
 Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala  
                   610                  615                  620  
 Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys  
                   625                  630                  635                  640  
 Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile  
                   645                  650                  655  
 Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr  
                   660                  665                  670  
 Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu  
                   675                  680                  685  
 His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val  
                   690                  695                  700  
 Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys  
                   705                  710                  715                  720

Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln  
725 730

<210> 58  
<211> 2205  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

| <400> | 58        |             |             |             |             |             |      |
|-------|-----------|-------------|-------------|-------------|-------------|-------------|------|
| atgc  | aactcc    | ttagcaaca   | gcagcaggaa  | gcagtatccg  | aaggcagcag  | cagcgggaga  | 60   |
| gcg   | aggggagg  | cctcgggggc  | tcccacttcc  | tccaaggaca  | attacttagg  | gggcacttcg  | 120  |
| acc   | atttctg   | acaacgccaa  | ggagttgtgt  | aaggcagtgt  | cggtgtccat  | gggcctgggt  | 180  |
| gtt   | ggggcgt   | tggagcatct  | gagtccaggg  | gaacagctc   | gggggattg   | catgtacgcc  | 240  |
| cc    | actttgg   | gagttccacc  | cgctgtgcgt  | cccactcctt  | gtgccccatt  | ggccgaatgc  | 300  |
| aa    | agggttctc | tgctagacga  | cagcgcaggc  | aagagcactg  | aagatactgc  | tgagtattcc  | 360  |
| cctt  | caagg     | gaggttacac  | caaaggcta   | gaaggcgaga  | gcctaggctg  | ctctggcagc  | 420  |
| gct   | gcagcag   | ggagctccgg  | gacacttcaa  | ctgcccgtcta | ccctgtctct  | ctacaagtcc  | 480  |
| gg    | gacttgg   | acgaggcagc  | tgcgtaccag  | agtcgcact   | actacaactt  | tccactggct  | 540  |
| ct    | ggccggac  | cggccccccc  | tccgcccct   | ccccatcccc  | acgctcgcat  | caagctggag  | 600  |
| aa    | accgcgtgg | actacggcag  | cgcctggcg   | gctgcccgg   | cgcagtgcgg  | ctatgggac   | 660  |
| ct    | ggcgagcc  | tgcattggcgc | gggtgcagcg  | ggacccgggt  | ctgggtcacc  | ctcagccgccc | 720  |
| gtt   | tcctcat   | cctggcacac  | tcttcaca    | gccgaagaag  | gccagttgt   | tggaccgtgt  | 780  |
| gg    | tggtgggtg | ggggtggtgg  | tggcggcggc  | ggcggcggcg  | gcccggcgg   | ccggcggcggc | 840  |
| gg    | ccggcggcg | ggggcggcgg  | cgaggcggaa  | gctgtagccc  | cctacggcta  | cactcggccc  | 900  |
| cct   | caggggc   | tggcgggcca  | ggaaagcgc   | tccaccgcac  | ctgatgtgt   | gtaccctggc  | 960  |
| gg    | catgggt   | gcagagtgc   | ctatcccagt  | ccacttgc    | tcaaaagcga  | aatggggccc  | 1020 |
| tgg   | atggata   | gtactccgg   | accttacggg  | gacatgcgtt  | tggagactgc  | cagggaccat  | 1080 |
| gtt   | ttggccca  | ttgactatta  | cttccaccc   | cagaagac    | gcctgatctg  | tggagatgaa  | 1140 |
| gtt   | ctgggtgg  | gtcactatgg  | agcttcaca   | tgtggaaagct | gcaaggctt   | cttcaaaaaga | 1200 |
| ggc   | gtcgtaag  | ggaaacagaa  | gtacctgtc   | gccagcagaa  | atgattgcac  | tattgataaa  | 1260 |
| ttcc  | gaagga    | aaaattgtcc  | atcttgcgt   | cttcggaaat  | gttatgaagc  | agggatgact  | 1320 |
| ctgg  | gagccc    | ggaagctgaa  | gaaacctgg   | aatctgaaac  | tacaggagga  | aggagaggct  | 1380 |
| tcc   | agcacca   | ccagccccac  | tgaggagaca  | acccagaagc  | tgacagtgtc  | acacattgaa  | 1440 |
| gg    | ctatgaaat | gtcagcccat  | ctttctgaat  | gtcttggaaag | ccattgagcc  | aggtgtagt   | 1500 |
| tgt   | gtggac    | acgacaacaa  | ccagccgcac  | tcctttgcag  | ccttgccttc  | tagcctcaat  | 1560 |
| ga    | actgggag  | agagacagct  | tgtacacgt   | gtcaagtgg   | ccaaaggcctt | gcctggcttc  | 1620 |
| cg    | caacttac  | acgtggacga  | ccagatggct  | gtcattca    | actctggat   | ggggctcatg  | 1680 |
| gt    | gtttgcca  | tggctggcg   | atccttcacc  | aatgtcaact  | ccaggatgt   | ctacttcgccc | 1740 |
| cct   | gtatctgg  | tttcaatga   | gtaccgcac   | cacaagtccc  | ggatgtacag  | ccagtgtgtc  | 1800 |
| cg    | aatgaggc  | acctctctca  | agagttgg    | tggctccaaa  | tcacccccc   | ggaattcctg  | 1860 |
| tg    | catgaaag  | cactgtact   | ttcagcatt   | attccagtg   | atgggctgaa  | aatcaaaaa   | 1920 |
| tt    | ctttgtat  | aacttgcata  | gaactacatc  | aaggaactcg  | atcgatcat   | tgcatgaaa   | 1980 |
| ag    | aaaaaaatc | ccacatctg   | ctcaagacgc  | ttctaccagc  | tcaccaagct  | cctggactcc  | 2040 |
| gt    | gcagccta  | ttgcgagaga  | gctgcacatc  | ttcacttttgc | acctgtctat  | caagtccacac | 2100 |
| at    | gggtgagcg | tggactttcc  | ggaaatgtat  | gcagagatca  | tctctgtgc   | agtgcaccaag | 2160 |
| at    | ccttctg   | ggaaagtcaa  | gccccatctat | ttccacaccc  | agtga       |             | 2205 |

```
<210> 59
<211> 216
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 59  
ccccagaaga cctgcctgat ctgtggagat gaagttctg ggtgtcacta tggagctctc 60  
acatgtggaa gctcaaggt cttttcaaa agagccgctg aaggaaaca gaagtacctg 120  
tgcgccagca gaaatgattt cactatttata aaattccgaa ggaaaaattt tccatcttgt 180  
cgcttcggaa aatgttatga agcagggatg actctg 216

<210> 60  
<211> 162  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 60  
ggagcccgga agctgaagaa acttggtaat ctgaaaactac aggaggaagg agaggcttcc 60  
agcaccacca gcccactga ggagacaacc cagaagctga cagtgtcaca cattgaaggc 120  
tatgaatgtc agcccatctt tctgaatgtc ctgaaagcca tt 162

<210> 61  
<211> 933  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 61  
Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly  
1 5 10 15  
Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala  
20 25 30  
Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val  
35 40 45  
Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys  
50 55 60  
Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu  
65 70 75 80  
Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala  
85 90 95  
Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp  
100 105 110  
Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln  
115 120 125  
Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly  
130 135 140  
Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val  
145 150 155 160  
Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser  
165 170 175  
Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala  
180 185 190  
Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala  
195 200 205  
Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu  
210 215 220  
Asp Gly Ser Glu Ser Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys  
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val  
                   245                  250                  255  
 Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp  
                   260                  265                  270  
 Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro  
                   275                  280                  285  
 Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile  
                   290                  295                  300  
 His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr  
                   305                  310                  315                  320  
 Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala  
                   325                  330                  335  
 Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro  
                   340                  345                  350  
 Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu  
                   355                  360                  365  
 Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala  
                   370                  375                  380  
 Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser  
                   385                  390                  395                  400  
 Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp  
                   405                  410                  415  
 Phe Pro Leu Gly Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser  
                   420                  425                  430  
 Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val  
                   435                  440                  445  
 Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys  
                   450                  455                  460  
 Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys  
                   465                  470                  475                  480  
 Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro  
                   485                  490                  495  
 Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr  
                   500                  505                  510  
 Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala  
                   515                  520                  525  
 Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr  
                   530                  535                  540  
 Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu  
                   545                  550                  555                  560  
 Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly  
                   565                  570                  575  
 Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys  
                   580                  585                  590  
 Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp  
                   595                  600                  605  
 Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu  
                   610                  615                  620  
 Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys  
                   625                  630                  635                  640  
 Lys Phe Asn Lys Val Arg Val Val Arg Ala Leu Asp Ala Val Ala Leu  
                   645                  650                  655  
 Pro Gln Pro Val Gly Val Pro Asn Glu Ser Gln Ala Leu Ser Gln Arg  
                   660                  665                  670  
 Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile  
                   675                  680                  685  
 Asn Leu Leu Met Ser Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp  
                   690                  695                  700  
 Asn Thr Lys Pro Asp Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln  
                   705                  710                  715                  720

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu  
 725 730 735  
 Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln  
 740 745 750  
 Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr  
 755 760 765  
 Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu  
 770 775 780  
 Asn Glu Gln Arg Met Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr  
 785 790 795 800  
 Met Trp Gln Ile Pro Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu  
 805 810 815  
 Glu Phe Leu Cys Met Lys Val Leu Leu Leu Asn Thr Ile Pro Leu  
 820 825 830  
 Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr  
 835 840 845  
 Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val  
 850 855 860  
 Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu  
 865 870 875 880  
 His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile  
 885 890 895  
 Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val  
 900 905 910  
 Ile Ala Ala Gln Leu Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu  
 915 920 925  
 Leu Phe His Lys Lys  
 930

<210> 62  
 <211> 3014  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 62  
 ctgaccagcg ccgcctccccc cggccccca cccaggaggt ggagatccct cccgtccagc 60  
 cacattcaac acccactttc tcctccctct gcccstatat tcccgaaacc ccctccctcct 120  
 tccctttcc ctcctccctg gagacggggg aggagaaaaag gggagtccag tcgtcatgac 180  
 ttagctgaag gcaaagggtc cccgggctcc ccacgtggcg ggccggccgc cctcccccg 240  
 ggtcgatcc ccactgctgt gtcgcccagc cgcaaggccg ttcccgggga gccagacacctc 300  
 ggacacctt cctgaagttt cggccatacc tatccctcg gacgggtcac tttccctcg 360  
 gccctgccag ggacaggacc cctccgacga aaagacgcag gaccagcagt cgctgtcgga 420  
 cttggagggc gcatattcca gagctgaagc tacaagggggt gctggaggca gcagttctag 480  
 tccccccagaa aaggacagcg gactgctgga cagtgcttgc gacactctgt tggccccc 540  
 agtccccggg cagagccaaac ccagccctcc cgcctgcgag gtcaccagct cttgggtgcct 600  
 gtttggccccc gaactccccg aagatccacc ggctgccccc gccaccacgc gggtgttgc 660  
 cccgctcatg agccgtccg ggtcaaggt tggagacacgc tccggacgg cagctgcccc 720  
 taaaagtgtcg cccccggggcc tgcaccacgc ccggcagctg ctgctcccg cctctgagag 780  
 ccctcaactgg tccggggccc cagtgaagcc gtctccgcgag gccgctgcgg tggagggttga 840  
 ggaggaggat ggctctgagt ccgaggagtc tgccgggtccg cttctgaagg gcaaaccctcg 900  
 ggctctgggt ggccggccgg ctggaggagg agccggggct gtcccgccgg gggccggcagc 960  
 aggaggcgtc gcccgggtcc ccaaggaaga ttcccgcttc tcagcgcaca gggtcgccc 1020  
 ggtggagcag gacgcggcga tggccggccg gcgctcccg ctggccacca cgggtatgg 1080  
 ttcatccac gtgcctatcc tgcctctcaa tcacgccta ttggcagccc gcaactcgca 1140  
 gctgctggaa gacgaaagtt acgacggccg ggccggggct gccagcgcct ttgccccgccc 1200  
 gccggagttca ccctgtgcct cgtccacccc ggtcgctgta ggcgacttcc cggactgcgc 1260  
 gtacccgccc gacgcgcgagc ccaaggacga cgcgtaccct ctctatacgq acttccagcc 1320

|             |              |             |             |             |             |      |
|-------------|--------------|-------------|-------------|-------------|-------------|------|
| gccccgtctta | aagataaaagg  | aggaggagga  | aggcgccggag | gcctccgcgc  | gctcccccgcg | 1380 |
| ttectacctt  | gtggccgggt   | ccaaccggc   | agccctcccg  | gattcccg    | tggggccacc  | 1440 |
| gcccccgctg  | ccggccgcag   | cgaccggatc  | cagaccgggg  | gaagggcg    | tgacggccgc  | 1500 |
| acccggccagt | gcctcagtct   | cgtctcggtc  | ctcctcgggg  | tcgaccctgg  | agtgcattct  | 1560 |
| gtacaaagcg  | gagggcgccg   | cgccccagca  | gggcccgttc  | gcccgcgc    | cctgcaaggc  | 1620 |
| gccccggcg   | agcggctgc    | tgcctcccg   | ggacggccgt  | ccctccacct  | ccgcctctgc  | 1680 |
| cgccgcgc    | ggggcgcccc   | ccgcgtctta  | ccctgcactc  | ggcctaacs   | ggctcccgca  | 1740 |
| gctcggtac   | caggcgcccc   | tgcctaagg   | gggcgtccg   | caggcttacc  | cgccctatct  | 1800 |
| caactacctg  | aggccggatt   | cagaagccag  | ccagagccca  | caatacagct  | tcgagtcatt  | 1860 |
| acctcagaag  | atttgtttaa   | tctgtgggga  | tgaagcatca  | ggctgtcatt  | atggtgtcct  | 1920 |
| tacctgtgg   | agctgttaagg  | tcttctttaa  | gagggcaatg  | gaagggcagc  | acaactactt  | 1980 |
| atgtgttga   | agaaaatgtact | gcatgttga   | taaaatccgc  | agaaaaaaact | gcccagcatg  | 2040 |
| tcgccttaga  | aagtgtgtc    | aggctggcat  | ggtccttgg   | ggtcggaaaat | ttaaaaagtt  | 2100 |
| caataaagtc  | agagttgtga   | gagcacttgg  | tgctgttgc   | ctcccacagc  | cagtggcg    | 2160 |
| tccaaatgaa  | agccaaagccc  | taagccagag  | attcaacttt  | tcaccaggc   | aagacataca  | 2220 |
| gtttagtcca  | ccactgtatca  | acctgttaat  | gagcattgaa  | ccagatgtga  | tctatgcagg  | 2280 |
| acatgacaac  | acaaaacctg   | acacctccag  | ttctttgtc   | acaagtctta  | atcaactagg  | 2340 |
| cgagagccaa  | cttctttcag   | tagtcaagt   | gtctaaatca  | ttgccagg    | tgcgaaactt  | 2400 |
| acatattgtat | gaccagataa   | ctctcattca  | gtattcttgg  | atgagcttaa  | ttgtgtttgg  | 2460 |
| tcttaggatgg | agatcctaca   | aacacgtcag  | ttggcagatg  | ctgtatttg   | cacctgatct  | 2520 |
| aataactaaat | gaacagcgga   | tgaaaagatc  | atcattctat  | tcattatgcc  | ttaccatgtg  | 2580 |
| gcagatccca  | caggagttt    | tcaagctca   | agtagccaa   | gaagagttcc  | tctgtatgaa  | 2640 |
| agtattgtta  | cttcttaata   | caattccctt  | ggaagggcta  | cgaagtcaaa  | cccagttga   | 2700 |
| ggagatgagg  | tcaagctaca   | ttagagagct  | catcaaggca  | attggttga   | ggcaaaaagg  | 2760 |
| agttgtgtcg  | agctcacagc   | gtttcttatca | acttacaaaa  | cttcttgata  | acttgcattga | 2820 |
| tcttgtcaaa  | caacttcattc  | tgtactgtt   | gaatacattt  | atccagttcc  | gggcactgag  | 2880 |
| tgttgaattt  | ccagaaatga   | tgtctgaagt  | tattgtctgca | caattacca   | agatattggc  | 2940 |
| agggtatgg   | aaaccccttc   | tcttcataa   | aaagtgaatg  | tcatctttt   | cttttaaaga  | 3000 |
| attaaatttt  | qtgg         |             |             |             |             | 3014 |

```
<210> 63
<211> 216
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

```

<400> 63
cctcagaaga tttgtttaat ctgtggggat gaagcatcag gctgtcatta tggtgtccctt      60
acctgtggga gctgttaaggc cttctttaag agggcaatgg aagggcagca caactactta      120
tgtgtggaa gaaatgactg catcggtataaaatccgca gaaaaaaactg cccagcatgt      180
cccccttagaa aqtgctgtca ggctggcatg gtcctt                                216

```

```
<210> 64
<211> 160
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 64 ggaggtcgaa aattnaaaaa gttcaataaaa gtcagagttg tgagagcact ggatgctgtt 60  
gctctccac agccagtggg cgttccaaat gaaagccaag ccctaagcca gagattcact 120  
ttttcaccaq qtcaaqacat acagttgatt ccaccactga 160

<210> 65  
<211> 455

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 65  
 Met Thr Glu Asn Gly Leu Thr Ala Trp Asp Lys Pro Lys His Cys Pro  
 1               5               10               15  
 Asp Arg Glu His Asp Trp Lys Leu Val Gly Met Ser Glu Ala Cys Leu  
 20              25              30  
 His Arg Lys Ser His Ser Glu Arg Arg Ser Thr Leu Lys Asn Glu Gln  
 35              40              45  
 Ser Ser Pro His Leu Ile Gln Thr Thr Trp Thr Ser Ser Ile Phe His  
 50              55              60  
 Leu Asp His Asp Asp Val Asn Asp Gln Ser Val Ser Ser Ala Gln Thr  
 65              70              75              80  
 Phe Gln Thr Glu Glu Lys Lys Cys Lys Gly Tyr Ile Pro Ser Tyr Leu  
 85              90              95  
 Asp Lys Asp Glu Leu Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr  
 100            105            110  
 His Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg  
 115            120            125  
 Thr Ile Gln Lys Asn Leu His Pro Ser Tyr Ser Cys Lys Tyr Glu Gly  
 130            135            140  
 Lys Cys Val Ile Asp Lys Val Thr Arg Asn Gln Cys Gln Glu Cys Arg  
 145            150            155            160  
 Phe Lys Lys Cys Ile Tyr Val Gly Met Ala Thr Asp Leu Val Leu Asp  
 165            170            175  
 Asp Ser Lys Arg Leu Ala Lys Arg Lys Leu Ile Glu Glu Asn Arg Glu  
 180            185            190  
 Lys Arg Arg Arg Glu Glu Leu Gln Lys Ser Ile Gly His Lys Pro Glu  
 195            200            205  
 Pro Thr Asp Glu Glu Trp Glu Leu Ile Lys Thr Val Thr Glu Ala His  
 210            215            220  
 Val Ala Thr Asn Ala Gln Gly Ser His Trp Lys Gln Lys Pro Lys Phe  
 225            230            235            240  
 Leu Pro Glu Asp Ile Gly Gln Ala Pro Ile Val Asn Ala Pro Glu Gly  
 245            250            255  
 Gly Lys Val Asp Leu Glu Ala Phe Ser His Phe Thr Lys Ile Ile Thr  
 260            265            270  
 Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Lys Leu Pro Met Phe  
 275            280            285  
 Cys Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly Cys Cys  
 290            295            300  
 Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro Glu Ser  
 305            310            315            320  
 Glu Thr Leu Thr Leu Asn Gly Glu Met Ala Val Ile Arg Gly Gln Leu  
 325            330            335  
 Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp Leu Gly  
 340            345            350  
 Met Ser Leu Ser Ser Phe Asn Leu Asp Asp Thr Glu Val Ala Leu Leu  
 355            360            365  
 Gln Ala Val Leu Leu Met Ser Ser Asp Arg Pro Gly Leu Ala Cys Val  
 370            375            380  
 Glu Arg Ile Glu Lys Tyr Gln Asp Ser Phe Leu Leu Ala Phe Glu His  
 385            390            395            400  
 Tyr Ile Asn Tyr Arg Lys His His Val Thr His Phe Trp Pro Lys Leu  
 405            410            415

Leu Met Lys Val Thr Asp Leu Arg Met Ile Gly Ala Cys His Ala Ser  
 420 425 430  
 Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Leu Pro Pro  
 435 440 445  
 Leu Phe Glu Val Phe Glu Asp  
 450 455

<210> 66  
<211> 1698  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 66  
cggcggggat caactttgca tgaataatgt gagtgcgctt ggaaaagaga cctcctgctc 60  
cgcgggctcg gggcaagagc ccgcaggcta ccttccccgg gcagggggcgc tcaacccaaac 120  
cggctccagg gcactgttaa tttggctaga ggaccgcgcg gaggcagcgg gatctgcgat 180  
ttccttctgg ttggctgtcc tgcgtgggtg ccaagttcca cacatgattt aatgaataag 240  
aaggagatgt cagtaaaaaa agggatccag aatgattact aacctataac ccccaacagt 300  
atgacagaaa atggcattac agcttggac aaaccgaagc actgtccaga ccgagaacac 360  
gactggaaagc tagtaggaat gtctgaagcc tgcctacata ggaagagcca ttcagagagg 420  
cgcagcacgt tgaaaaatga acagtcgtcg ccacatctca tccagaccac ttggactagc 480  
tcaaataattcc atctggacca tcatgtatgt aacgaccaga gtgtctcaag tgcccagacc 540  
ttccaaacgg aggagaagaa atgtaaaggg tacatccccca gttacttaga caaggacgag 600  
ctctgtgtag tgggtgtga caaagccacc gggtatcact accgctgtat cacgtgtgaa 660  
ggctgcaagg gtttcttttag aagaaccatt cagaaaaatc tccatccatc ctattcctgt 720  
aaatatgaag gaaaatgtgt catagacaaa gtcacgcgaa atcagtgcga ggaatgtcgc 780  
ttaagaaat gcatctatgt tggcatggca acagatttg tgctggatga cagcaagagg 840  
ctggccaaga ggaagctgat agaggagaac cgggagaaaa gacggcggga agagctgcag 900  
aagtccatcg ggcacaagcc agagccaca gacgaggaat gggagctcat caaaactgtc 960  
accgaagccc atgtggcgac caacgccccaa ggcagccact ggaagcaaaa accgaaattt 1020  
ctgccagaag acattggaca agcacaata gtcaatgccc cagaagggtgg aaaggttgac 1080  
tttggagcc tcagccattt tacaaaaatc atcacaccag caattaccag agtgggtggat 1140  
tttgcAAAA agttgcctat gtttgtgag ctggcatgt aagaccagat catcctcctc 1200  
aaaggctgct gcatggagat catgtccctt cgcgctgctg tgctgtatga cccggaaagt 1260  
gagactttaa ctttgaatgg gaaaatggca gtgatacggg gccagctgaa aatgggggt 1320  
cttgggtgg tgcagacgc catcttgcac ctggcatgt ctctgtcttc ttcaacctg 1380  
gatgacactg aagtggccct ctttcaggcc gtcctgctga tgcgttccaga tcgccccggg 1440  
cttgcctgtg ttgagagaat agaaaagtagc caagatagtt tcctgctggc cttgaacac 1500  
tatatcaatt accgaaaaca ccacgtgaca cactttggc caaaactcct gatgaagggtg 1560  
acagatctgc ggatgatagg agcctgcccat gccagccgt tcctgcacat gaaggtggaa 1620  
tgccccacag aactcctccc cccttggtc ctggaaagtgt tcgaggatta gactgactgg 1680  
attccttcctt ataattcc 1698

<210> 67  
<211> 216  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 67  
aaggacgagc tctgtgttagt gtgtgggtgac aaagccaccg ggtatcacta ccgctgtatc 60  
acgtgtgaag gctgcaaggg tttcttttaga agaaccattc agaaaaatct ccatccatcc 120  
tattcctgtta aatatgaagg aaaatgtgtc atagacaaag tcacgcgaaa tcagtgcac 180  
gaatgtcgct ttaagaaatg catctatgtt ggcattt 216

```

<210> 68
<211> 189
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 68
gcaacagatt tggtgctgga tgacagcaag aggctggcca agaggaagct gatagaggag 60
aaccgggaga aaagaacggcg ggaagagctg cagaagtcca tcgggcacaa gccagagccc 120
acagacgagg aatgggagct catcaaact gtcaccgaag cccatgtggc gaccaacgcc 180
caaggcagc 189

<210> 69
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 69
Met Asp Thr Lys His Phe Leu Pro Leu Asp Phe Ser Thr Gln Val Asn
 1           5          10          15
Ser Ser Leu Thr Ser Pro Thr Gly Arg Gly Ser Met Ala Ala Pro Ser
 20          25          30
Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln Leu His
 35          40          45
Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly Pro Pro
 50          55          60
Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser Val Pro
 65          70          75          80
Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu Ser Ser
 85          90          95
Pro Met Asn Pro Val Ser Ser Glu Asp Ile Lys Pro Pro Leu Gly
 100         105         110
Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn Met Ala
 115         120         125
Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly
 130         135         140
Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys
 145         150         155         160
Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp
 165         170         175
Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr
 180         185         190
Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln Glu Glu
 195         200         205
Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser Thr Ser
 210         215         220
Ser Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu
 225         230         235         240
Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu
 245         250         255
Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala
 260         265         270

```

Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His  
 275 280 285  
 Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly  
 290 295 300  
 Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val  
 305 310 315 320  
 Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser  
 325 330 335  
 Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu  
 340 345 350  
 Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly  
 355 360 365  
 Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser  
 370 375 380  
 Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu  
 385 390 395 400  
 Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala  
 405 410 415  
 Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys  
 420 425 430  
 Leu Glu His Leu Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp  
 435 440 445  
 Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr  
 450 455 460

<210> 70  
 <211> 5449  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 70  
 ggcgggggg cggccgcgcc cgccgccccgc tgcctgcgcc gccggccggg catgagtttag 60  
 tcgcagacat ggacacaaaa catttcctgc cgctcgattt ctccacccag gtgaactcct 120  
 ccctcacctc cccgacgggg cgaggctcca tggctgcccc ctcgctgcac ccgtccctgg 180  
 ggcctggcat cggctccccg ggacagctgc attctccat cagcacccctg agctccccca 240  
 tcaacggcat gggccggcct ttctcggtca tcagctcccc catggggcccc cactccatgt 300  
 cggtgcccac cacacccacc ctgggcttca gcactggcag ccccccagctc agctcaccta 360  
 tgaaccctcgat cagcagcgc gaggacatca agccccccct gggcctcaat ggcgtccctca 420  
 aggtccccgc ccacccctca gaaaacatgg cttccttcac caagcacatc tgcccatct 480  
 gccccggaccg ctccctcaggc aagcactatg gagtgtacag ctgcgagggg tgcaaggggct 540  
 tcttcaagcg gacgggtgcgc aaggacctga cctacacctg cccgcacaac aaggactgcc 600  
 tgattgacaa gcccgcggg aaccgggtgcc agtactgccg ctaccagaag tgcctggcca 660  
 tgggcattgaa gcccggaaagcc gtgcaggagg agcggcagcg tggcaaggac cggAACGAGA 720  
 atgaggtggaa gtcgaccgc agcgccaaacg aggacatgc ggtggagagg atccctggagg 780  
 ctgagctggc cgtggagccc aagaccgaga cctacgtgg aacggactgccc 840  
 ccagctgcgc gaacgaccct gtcaccaaca tttgccaagc agccgacaaa cagctttca 900  
 ccctgggtggaa gtggggccaag cggatcccac acttctcaga gctccctcg gacgaccagg 960  
 tcatacctget gccccggcaggc tggaatgagc tgctcatcgc ctcccttcaccgcgtccca 1020  
 tgcggcgtgaa ggacggggatc ctccctggcca cccggctgca cgtccacccgg aacagcgccc 1080  
 acagcgcagg ggtggggcgc atcttgcaca ggggtctgac ggagcttgc tccaagatgc 1140  
 gggacatgca gatggacaag acggagctgg gctgcctgca cgccatcgcc ctcttttaacc 1200  
 ctgactccaa ggggctctcg aacccggccg aggtggaggc gctgaggagg aaggctatg 1260  
 cgtcccttggaa ggcctactgc aagcacaagt acccagagca gccggaaagg ttgcctaagc 1320  
 tcttgcctcg cctggccggct ctgcgcgtccaa tcgggctcaa atgcctggaa catctttct 1380  
 tcttcaaget catcggggac acacccattg acaccccttatg tattggagatg ctggaggcgc 1440  
 cgccaccaat gacttaggccc tcctttgtgc ccacccgttc tgccaccct 1500

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| gcctggacgc  | cagctgttct | tctcagcctg | agccccgttcc | ctggcccttct | ctgcctggcc  | 1560 |
| tgtttggact  | ttggggcaca | gcctgtca   | gctctgccta  | agagatgtgt  | tgtcacccctc | 1620 |
| cttatttctg  | ttactacttg | tctgtggccc | agggcagtgg  | cttccctgag  | gcagcagcct  | 1680 |
| tcgtggcaag  | aactagcgtg | agcccagcca | ggcgcctccc  | caccgggctc  | tcaggacacc  | 1740 |
| ctgccacacc  | ccacggggct | tggcgacta  | cagggtcttc  | gggccccagc  | cctggagctg  | 1800 |
| caggagttgg  | gaacggggct | tttgc      | tttgc       | tttgc       | tttca       | 1860 |
| tcctgtgtgg  | ccctcctgtc | tggagtgaca | tcttc       | tctga       | tgg         | 1920 |
| ccagccgtg   | acagttccc  | ccta       | atcagg      | aggggacagc  | ttggggcgca  | 1980 |
| tcatca      | aa         | agac       | ctc         | ag          | caag        | 2040 |
| gcctgtgt    | ct         | gag        | tt          | gggg        | caag        | 2100 |
| gcctcgagc   | caat       | gaga       | at          | gat         | ca          | 2160 |
| gctgcagggg  | cgg        | gtact      | ccccc       | tttct       | ca          | 2220 |
| actcccact   | cccc       | gttca      | cc          | ctc         | ca          | 2280 |
| ttgc        | tcg        | gggtggg    | gg          | tttct       | cc          | 2340 |
| gcagggtggg  | gcat       | cacc       | ct          | act         | cc          | 2400 |
| cagccatctg  | tgagg      | cccc       | ggggat      | gggg        | tttcc       | 2460 |
| agagggggca  | gg         | ggc        | tttgc       | gggg        | gggg        | 2520 |
| cagatgtcc   | gg         | ggc        | tttgc       | gggg        | gggg        | 2580 |
| ttctctctgg  | ct         | cc         | tttgc       | gggg        | gggg        | 2640 |
| gcgc        | cc         | ct         | gggg        | gggg        | gggg        | 2700 |
| acggacagcg  | tt         | tt         | cc          | tttgc       | gggg        | 2760 |
| tgaagggtggg | gt         | gggg       | gggg        | gggg        | gggg        | 2820 |
| tc          | cc         | cc         | gggg        | gggg        | gggg        | 2880 |
| gcctcttt    | ca         | ct         | gggg        | gggg        | gggg        | 2940 |
| gtcccgtg    | cc         | cc         | gg          | gggg        | gggg        | 3000 |
| tac         | cc         | cc         | gg          | gggg        | gggg        | 3060 |
| cttctccata  | gt         | ttt        | cc          | gggg        | gggg        | 3120 |
| ta          | cc         | cc         | gggg        | gggg        | gggg        | 3180 |
| ta          | cc         | cc         | gggg        | gggg        | gggg        | 3240 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3300 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3360 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3420 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3480 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3540 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3600 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3660 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3720 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3780 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3840 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3900 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 3960 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4020 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4080 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4140 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4200 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4260 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4320 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4380 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4440 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4500 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4560 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4620 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4680 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4740 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4800 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4860 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4920 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 4980 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 5040 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 5100 |
| cc          | cc         | cc         | gggg        | gggg        | gggg        | 5160 |

|   |      |
|---|------|
| gggcctgagg cttcaaggg ttttctccc ttccgatcaa ttttaaagc cttgctctgt    | 5220 |
| tgtgtcctgt tgccggctct ggccttcctg tgactgactg tgaagtggct tctccgtacg | 5280 |
| attgtctctg aaacatcggt gcctcaggtg ccagggttt atggacagta gcattagaat  | 5340 |
| tgtggaaaag gaacacgcaa agggagaagt gtgagaggag aaacaaaata tgagcggtta | 5400 |
| aaatacatcg ccattcagtt cgtaaaaaaaaaaaaaaa                          | 5449 |

<210> 71  
<211> 210  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

|   |     |
|---|-----|
| <400> 71  |     |
| accaagcaca tctgcgccat ctgcggggac cgctcctcag gcaaggacta tggagtgtac | 60  |
| agctgcagg ggtcaaggg cttcttcaag cggacgggtgc gcaaggacct gacctacacc  | 120 |
| tgccgcgaca acaaggactg cctgattgac aagcggcagc ggaaccggtg ccagtactgc | 180 |
| cgctaccaga agtgctggc catgggcatg                                   | 210 |

<210> 72  
<211> 177  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

|   |     |
|---|-----|
| <400> 72  |     |
| aagcggaaag ccgtgcagga ggagcggcag cgtggcaagg accggaacga gaatgaggtg | 60  |
| gagtcgacca gcagcgc当地 cgaggacatg ccgtggaga ggatcctgga ggctgagctg   | 120 |
| cccgtagc ccaagaccga gacctacgtg gaggcaaaca tggggctgaa cccccacc     | 177 |

<210> 73  
<211> 462  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

|   |  |
|---|--|
| <400> 73  |  |
| Met Ala Ser Asn Ser Ser Ser Cys Pro Thr Pro Gly Gly Gly His Leu |  |
| 1 5 10 15   |  |
| Asn Gly Tyr Pro Val Pro Pro Tyr Ala Phe Phe Phe Pro Pro Met Leu |  |
| 20 25 30  |  |
| Gly Gly Leu Ser Pro Pro Gly Ala Leu Thr Thr Leu Gln His Gln Leu |  |
| 35 40 45  |  |
| Pro Val Ser Gly Tyr Ser Thr Pro Ser Pro Ala Thr Ile Glu Thr Gln |  |
| 50 55 60  |  |
| Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro Pro Pro |  |
| 65 70 75 80   |  |
| Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser |  |
| 85 90 95  |  |
| Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly Phe Phe |  |
| 100 105 110   |  |

Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg Asp Lys  
 115 120 125  
 Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr Cys Arg  
 130 135 140  
 Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val Arg Asn  
 145 150 155 160  
 Asp Arg Asn Lys Lys Lys Glu Val Pro Lys Pro Glu Cys Ser Glu  
 165 170 175  
 Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys Val Arg  
 180 185 190  
 Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly Lys Tyr  
 195 200 205  
 Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile Asp Leu  
 210 215 220  
 Trp Asp Lys Phe Ser Glu Leu Ser Thr Lys Cys Ile Ile Lys Thr Val  
 225 230 235 240  
 Glu Phe Ala Lys Gln Leu Pro Gly Phe Thr Thr Leu Thr Ile Ala Asp  
 245 250 255  
 Gln Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Ile Leu Arg  
 260 265 270  
 Ile Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe Ser Asp  
 275 280 285  
 Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe Gly Pro  
 290 295 300  
 Leu Thr Asp Leu Val Phe Ala Phe Ala Asn Gln Leu Leu Pro Leu Glu  
 305 310 315 320  
 Met Asp Asp Ala Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu Ile Cys  
 325 330 335  
 Gly Asp Arg Gln Asp Leu Glu Gln Pro Asp Arg Val Asp Met Leu Gln  
 340 345 350  
 Glu Pro Leu Leu Glu Ala Leu Lys Val Tyr Val Arg Lys Arg Arg Pro  
 355 360 365  
 Ser Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr Asp Leu  
 370 375 380  
 Arg Ser Ile Ser Ala Lys Gly Ala Glu Arg Val Ile Thr Leu Lys Met  
 385 390 395 400  
 Glu Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu Glu Asn  
 405 410 415  
 Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly Arg  
 420 425 430  
 Asp Gly Gly Leu Ala Pro Pro Gly Ser Cys Ser Pro Ser Leu  
 435 440 445  
 Ser Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro  
 450 455 460

<210> 74  
 <211> 2907  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 74  
 gccatctggg cccaggcccc atgccccgag gaggggtggt ctgaagccca ccagagcccc 60  
 ctgcggagact gtctgcctcc ttctgactg tggccgcttg gcatggccag caacagcagc 120  
 tcctggccga cacctggggg cgggcacctc aatgggtacc cggtgcctcc ctacgccttc 180  
 ttcttccccc ctatgctggg tggactctcc ccggcaggcg ctctgaccac tctccagcac 240  
 cagttcccaag ttagtgttata tagcacacca tccccagcca ccattgagac ccagagcagc 300  
 agttctgaag agatagtgcc cagccctcccc ctctaccccg catctacaag 360

|   |      |
|---|------|
| ccttgctttg tctgtcagga caagtcctca ggctaccact atggggtcag cgccctgttag  | 420  |
| ggctgcaagg gcttcttcg ccgcagcatc cagaagaaca tggtgtacac gtgtcaccgg    | 480  |
| gacaagaact gcatcatcaa caaggtgacc cggAACGCT gccagtactg ccgactgca     | 540  |
| aagtgcTTTg aagtggcat gtccaaggag tctgtgagaa acgaccgaaa caagaagaag    | 600  |
| aaggaggtgc ccaagcccga gtgctctgag agtacacgc tgacGCCGA ggtggggag      | 660  |
| ctcattgaga aggtgcgaa agcgcaccag gaaaccttc ctgcctctg ccagctggc       | 720  |
| aaatacacta cgaacaacag ctcagaacaa cgtgtctc tggacattga cctctggac      | 780  |
| aagttcagtg aactctccac caagtgcac attaagactg tggagTCGC caagcagctg     | 840  |
| cccggttca ccacccctcac catGCCGAC cagatcaccc tcctcaaggc tgccTgcctg    | 900  |
| gacatcctga tcctgcggat ctgcacgcgg tacacGCCG agcaggacac catgaccttc    | 960  |
| tcggacgggc tgaccctgaa cggaccagg atgcacaacg ctggcttcgg cccccctcacc   | 1020 |
| gacctggct ttgcctcgc caaccagctg ctgcccctgg agatggatga tgcggagacg     | 1080 |
| gggctgctca ggcacatctg cctcatctgc ggagaccgccc aggacctgga gcagccggac  | 1140 |
| cgggtggaca tgctgcagga gccgctgtg gaggccta aggtctacgt gccgaagcgg      | 1200 |
| aggcccagcc gccccacat ttcccccaag atgctaattga agattactga cctgcgaagc   | 1260 |
| atcagcgcca agggggctga ggggtgatc acgctgaaga tggagatccc gggctccatg    | 1320 |
| ccgcctctca tccagggaaat gttggagaac tcagagggcc tggacactct gagcggacag  | 1380 |
| ccgggggggtg gggggcggga cgggggtggc ctggcccccc cgccaggcag ctgtagcccc  | 1440 |
| agcctcagcc ccagctccaa cagaaggcgc cggccaccc actcccgtg accgcccacg     | 1500 |
| ccacatggac acagccctcg ccctccggcc cggctttct ctgccttct accgaccatg     | 1560 |
| tgaccccgca ccagccctgc ccccacctgc cctccggc agtactggg accttccctg      | 1620 |
| ggggacgggg agggaggagg cagcactcc ttggacagag gcctggcccc tcagtggact    | 1680 |
| gcctgctccc acagcctggg ctgacgtcag agggcgaggc caggaactga gtgaggcccc   | 1740 |
| tggctctggg tctcaggatg ggtcctgggg gcctcgtgtt catcaagaca cccctctgcc   | 1800 |
| cagctcacca catttcatc accagcaaa gccaggactt ggctccccca tcctcagaac     | 1860 |
| tcacaagcca ttgctccca gctggggaa ctcaacctcc cccctgcctc gttgggtgac     | 1920 |
| agaggggggtg ggacaggggc ggggggttcc ccctgtacat accctgcctt accaacccca  | 1980 |
| ggtattaatt ctcgtctgtt ttgttttat ttaattttt ttgtttgtat ttttttaata     | 2040 |
| agaattttca ttttaagcac atttatactg aagaatttg tgctgtgtat tggggggagc    | 2100 |
| tggatccaga gctggagggg gtgggtccgg gggaggagg ggtcgaaag gggccccac      | 2160 |
| tctctttca tgcctctgtg ccccccagtt ctccctctca gcctttccct ctcagtttt     | 2220 |
| ctctttaaaaa ctgtgaagta ctaactttcc aaggcctgcc tteccctccc tcccactgga  | 2280 |
| gaagccgcca gccccttct ccctctgcct gaccactggg tgtggacggt gtggggcagc    | 2340 |
| cctgaaagga caggtcctg gcctggcac ttgcctgcac ccaccatgag gcatggagca     | 2400 |
| gggcagagca agggccccgg gacagagtt tcccagaccc ggctcctcg cagagctgcc     | 2460 |
| tcccgtcagg gcccacatca tctaggctcc ccagccccca ctgtgaaggg gctggccagg   | 2520 |
| ggcccggagct gcccacaccc cgggcctcag ccaccagcac ccccataggg cccccagaca  | 2580 |
| ccacacacat ggcgtgcgc acacacacaa acacacacac actggacagt agatggccg     | 2640 |
| acacacacat ggcccgagtt ctcatttc cctggctgc ccccccaccc caacctgtcc      | 2700 |
| caccccccgtg cccctctctt accccgcaagg acgggctac aggggggtct cccctcaccc  | 2760 |
| ctgcacccccc agctggggga gctggctctg ccccgacctc cttcaccagg gttggggcc   | 2820 |
| ccttccccctg gagcccggtgg gtgcacctgt tactgttggg ctttccactg agatctactg | 2880 |
| gataaagaat aaaggcttat ttattct                                       | 2907 |

&lt;210&gt; 75

&lt;211&gt; 216

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 75

|  |     |
|--|-----|
| atctacaagc cttgtttgt ctgtcaggac aagtctcag gctaccacta tggggtcagc    | 60  |
| gcctgtgagg gctgcaaggg cttcttcgc cgcagcatcc agaagaacat ggtgtacacg   | 120 |
| ctgtcaccggg acaagaactg catcatcaac aaggtgaccc ggaaccgctg ccagtactgc | 180 |
| cgactgcaga agtgcattga agtgggcattg tccaaag                          | 216 |

&lt;210&gt; 76

&lt;211&gt; 207

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 76  
 gagtctgtga gaaacgaccg aaacaagaag aagaaggagg tgcccaagcc cgagtgcctc       60  
 gagagctaca cgctgacgcc ggaggtgggg gagctcattg agaaggtgcg ccaaagcgcac     120  
 cagggaaacct tccctgcccct ctgccagctg ggcaaataca ctacgaacaa cagctcagaa   180  
  
 caacgtgtct ctctggacat tgacctc   207

<210> 77  
 <211> 427  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 77  
 Met Glu Ala Met Ala Ala Ser Thr Ser Leu Pro Asp Pro Gly Asp Phe  
 1               5   15  
 Asp Arg Asn Val Pro Arg Ile Cys Gly Val Cys Gly Asp Arg Ala Thr  
 20               25   30  
 Gly Phe His Phe Asn Ala Met Thr Cys Glu Gly Cys Lys Gly Phe Phe  
 35               40   45  
 Arg Arg Ser Met Lys Arg Lys Ala Leu Phe Thr Cys Pro Phe Asn Gly  
 50               55   60  
 Asp Cys Arg Ile Thr Lys Asp Asn Arg Arg His Cys Gln Ala Cys Arg  
 65               70   80  
 Leu Lys Arg Cys Val Asp Ile Gly Met Met Lys Glu Phe Ile Leu Thr  
 85               90   95  
 Asp Glu Glu Val Gln Arg Lys Arg Glu Met Ile Leu Lys Arg Lys Glu  
 100              105   110  
 Glu Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys Leu Ser Glu Glu Gln  
 115              120   125  
 Gln Arg Ile Ile Ala Ile Leu Leu Asp Ala His His Lys Thr Tyr Asp  
 130              135   140  
 Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro Pro Val Arg Val Asn  
 145              150   160  
 Asp Gly Gly Ser His Pro Ser Arg Pro Asn Ser Arg His Thr Pro  
 165              170   175  
 Ser Phe Ser Gly Asp Ser Ser Ser Cys Ser Asp His Cys Ile Thr  
 180              185   190  
 Ser Ser Asp Met Met Asp Ser Ser Phe Ser Asn Leu Asp Leu Ser  
 195              200   205  
 Glu Glu Asp Ser Asp Asp Pro Ser Val Thr Leu Glu Leu Ser Gln Leu  
 210              215   220  
 Ser Met Leu Pro His Leu Ala Asp Leu Val Ser Tyr Ser Ile Gln Lys  
 225              230   240  
 Val Ile Gly Phe Ala Lys Met Ile Pro Gly Phe Arg Asp Leu Thr Ser  
 245              250   255  
 Glu Asp Gln Ile Val Leu Leu Lys Ser Ser Ala Ile Glu Val Ile Met  
 260              265   270  
 Leu Arg Ser Asn Glu Ser Phe Thr Met Asp Asp Met Ser Trp Thr Cys  
 275              280   285

Gly Asn Gln Asp Tyr Lys Tyr Arg Val Ser Asp Val Thr Lys Ala Gly  
 290 295 300  
 His Ser Leu Glu Leu Ile Glu Pro Leu Ile Lys Phe Gln Val Gly Leu  
 305 310 315 320  
 Lys Lys Leu Asn Leu His Glu Glu His Val Leu Leu Met Ala Ile  
 325 330 335  
 Cys Ile Val Ser Pro Asp Arg Pro Gly Val Gln Asp Ala Ala Leu Ile  
 340 345 350  
 Glu Ala Ile Gln Asp Arg Leu Ser Asn Thr Leu Gln Thr Tyr Ile Arg  
 355 360 365  
 Cys Arg His Pro Pro Pro Gly Ser His Leu Leu Tyr Ala Lys Met Ile  
 370 375 380  
 Gln Lys Leu Ala Asp Leu Arg Ser Leu Asn Glu Glu His Ser Lys Gln  
 385 390 395 400  
 Tyr Arg Cys Leu Ser Phe Gln Pro Glu Cys Ser Met Lys Leu Thr Pro  
 405 410 415  
 Leu Val Leu Glu Val Phe Gly Asn Glu Ile Ser  
 420 425

&lt;210&gt; 78

&lt;211&gt; 1284

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 78

|             |             |            |               |             |             |      |
|-------------|-------------|------------|---------------|-------------|-------------|------|
| atggaggccaa | tggcgcccaag | cacttccctg | cctgaccctg    | gagactttga  | ccggAACgtg  | 60   |
| ccccggatct  | gtggggtgtg  | tggagaccga | gcacactggct   | ttcacttcaa  | tgctatgacc  | 120  |
| tgtgaaggct  | gcaaaggctt  | cttcaggcga | agcatgaagc    | ggaaggcact  | attcacctgc  | 180  |
| cccttcaacg  | gggactgccc  | catcacaag  | gacaaccgac    | gccactgcca  | ggcctgcccgg | 240  |
| ctcaaacgct  | gtgtggacat  | cggcatgatg | aaggagttca    | ttctgacaga  | tgaggaagtg  | 300  |
| cagaggaagc  | gggagatgat  | cctgaagcgg | aaggaggagg    | aggccttcaa  | ggacagtctg  | 360  |
| cggcccaagc  | tgtctgagga  | gcagcagcgc | atcattgcca    | tactgctgga  | cggccaccat  | 420  |
| aagacctacg  | accccaccta  | ctccgacttc | tgccagttcc    | ggcctccagt  | tcgtgtgaat  | 480  |
| gatggtggag  | ggagccatcc  | ttccagccc  | aactccagac    | acactcccag  | tttctctggg  | 540  |
| gactcctcct  | cctcctgctc  | agatcactgt | atcacctctt    | cagacatgat  | ggactcggtcc | 600  |
| agtttctcca  | atctggatct  | gagtgaagaa | gattcagatg    | accctctgt   | gacccttagag | 660  |
| ctgtcccaagc | tctccatgct  | gccccacctg | gctgacctgg    | tcaatttacag | catccaaaag  | 720  |
| gtcattggct  | ttgctaagat  | gataccagga | ttcagagacc    | tcacctctga  | ggaccagatc  | 780  |
| gtactgctga  | agtcaagtgc  | cattgaggc  | atcatgttgc    | gctccaatga  | gtccttcacc  | 840  |
| atggacgaca  | tgtcctggac  | ctgtggcaac | caagactaca    | agtaccgcgt  | cagtgacgtg  | 900  |
| acccaaagccg | gacacagcct  | ggagctgatt | gagccccctca   | tcaatttcca  | ggtgggactg  | 960  |
| aagaagctga  | acttgcata   | ggaggagcat | gtcctgctca    | tggccatctg  | catcgcttcc  | 1020 |
| ccagatcgta  | ctggggtgca  | ggacgcccgc | ctgattgagg    | ccatccagga  | ccgcctgtcc  | 1080 |
| aacacactgc  | agacgtacat  | ccgctgccgc | cacccgcccc    | cgggcagcca  | cctgctctat  | 1140 |
| gccaagatga  | tccagaagct  | agccgacctg | cgccgctca     | atgaggagca  | ctccaagcag  | 1200 |
| taccgctgcc  | tctccttcca  | gcctgagtg  | gc agcatgaagc | taacgcccct  | tgtgctcgaa  | 1260 |
| gtgtttggca  | atgagatctc  | ctgta      |               |             |             | 1284 |

&lt;210&gt; 79

&lt;211&gt; 210

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

```

<400> 79
cgatctgtg gggtgtgtgg agaccgagcc actggcttc acttcaatgc tatgacctgt      60
gaaggctgca aaggcttctt caggcgaagc atgaagcgg aaggcactatt cacctgcccc      120
ttcaacgggg actgccgcat caccaaggac aaccgacgccc actgcccaggc ctgcccggctc      180
aacgcgtgtg tggacatcg catgatgaag                                210

<210> 80
<211> 195
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 80
gagttcattc tgacagatga ggaagtgcag aggaagcggg agatgatcct gaagcggaaag      60
gaggaggagg ccttgaagga cagtctgcgg cccaagctgt ctgaggagca gcagcgcatac      120
attgccatac tgctggacgc ccaccataag acctacgacc ccacctaactc cgacttctgc      180
cagttccggc ctcca                                195

<210> 81
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 81
Met Lys Gly Gly Val Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys
 1           5           10          15
His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
 20          25          30
Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile
 35          40          45
Lys Arg Ser
 50

<210> 82
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 82
Met Ala Arg Arg Pro Arg His Ser Ile Tyr Ser Ser Asp Glu Asp Asp
 1           5           10          15
Glu Asp Phe Glu Met Cys Asp His Asp Tyr Asp Gly Leu Leu Pro Lys
 20          25          30
Ser Gly Lys Arg His Leu Gly Lys Thr Arg Trp Thr Arg Glu Glu
 35          40          45

<210> 83
<211> 71
<212> DNA
<213> Artificial Sequence

```

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 83  
ctctggatcc ggtggaggtg gttctggagg aggtggttcc ggaggtggag gaaaggagac 60  
gcgttacgct g 71

<210> 84  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 84  
Leu Trp Ile Arg Trp Arg Trp Phe Trp Arg Arg Trp Phe Arg Arg Trp  
1 5 10 15  
Arg Lys Gly Asp Ala Leu Thr Leu  
20